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August 10, 2004

Linda S. Evans
Johnson & Johnson
One Johnson & Johnson Plaza
New Brunswick, NJ 08933-7003

In re application of:
Darrow et al
No.: 10/015,989
Filed: December 10, 2001
For: Zymogen Activation System

In response to the petition received on February 26, 2004, to withdraw the holding of abandonment in the above application. A copy of the sequence list sent March 25, 2002, has not reached the application. Enclosed is a copy of the raw sequence listing error report.
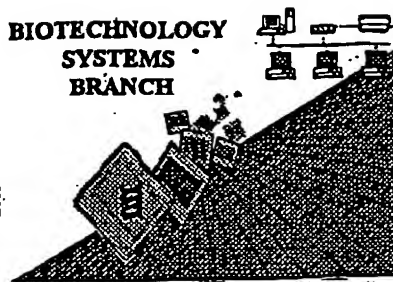
Please submit these documents to complete the application.

Telephone inquiries concerning this matter may be directed to Doshie E. Day at (703) 308-3640.

Doshie E. Day
Program Management Assistant
Office Initial Patent Examination

BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _/o/o/5,989_
Source: _OIPE_
Date Processed by STIC: _1/3/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:
1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission
   User Manual - ePAVE)
2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
   Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
                Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
   2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
   Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/015,989

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWAF

1 ____ Wrapped Nucleics
      Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

· 2 ____ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino
      Numbering
The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length
Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0
      "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences
      (OLD RULES)
Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences
      (NEW RULES)
Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's
      (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10 ____ Invalid <213>
       Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0
       "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

```
            RAW SEQUENCE LISTING                    DATE: 01/03/2002
            PATENT APPLICATION:  US/10/015,989      TIME: 15:41:56

            Input Set : A:\ES.txt
            Output Set: N:\CRF3\01032002\J015989.raw
```

see item 4 on Error Summary Sheet

```
      7 <110> APPLICANT: DARROW, ANDREW
     10        QI, JENSON
     13        ANDRADE-GORDON, PATRICIA
     19 <120> TITLE OF INVENTION: ZYMOGEN ACTIVATION SYSTEM
     25 <130> FILE REFERENCE: ORT-1552
     31 <140> CURRENT APPLICATION NUMBER: US/10/015,989
     34 <141> CURRENT FILING DATE: 2001-12-10
     40 <160> NUMBER OF SEQ ID NOS: 60
     46 <170> SOFTWARE: PATENTIN VER. 2.0
```

Does Not Comply *pp 1-12*
Corrected Diskette Needed

ERRORED SEQUENCES

FYI! nucleotides must be in lower-case letters when Sequence Listing is in new Sequence Rules format

```
     52 <210> SEQ ID NO: 1
     55 <211> LENGTH: 361
     58 <212> TYPE: DNA
     61 <213> ORGANISM: ARTIFICIAL SEQUENCE
     67 <220> FEATURE:
     70 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
     73        VECTORS.
     79 <400> SEQUENCE: 1
E--> 82 gaattcacca ccatggacag caaaggttcg tcgcagaaat cccgcctgct
     83 cctgctgctg 60
E--> 86 gtggtgtcaa atctactctt gtgccagggt gtggtctccg actacaagga
     87 cgacgacgac 120
E--> 90 gtggacgcgg ccgctcttgc tgcccccttt gatgatgatg acaagatcgt
     91 tggggggctat 180
E--> 94 gctctagata gcggccgctt cccctttagtg agggttaatg cttcgagcag
     95 acatgataag 240
E--> 98 atacattgat gagtttggac aaaccacaac tagaatgcag tgaaaaaaat
     99 gctttatttg 300
E--> 102 tgaaatttgt gatgctattg ctttatttgt aaccattata agctgcaata
    103 aacaagttga 360
    106 c                                        361
```

format (see error item 1 on Error Summary Sheet)

60 ← *format*
120 ←

```
    112 <210> SEQ ID NO: 2
    115 <211> LENGTH: 301
    118 <212> TYPE: DNA
    121 <213> ORGANISM: ARTIFICIAL SEQUENCE
    127 <220> FEATURE:
    130 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
    133        VECTORS.
    139 <400> SEQUENCE: 2
E--> 142 gaattcacca tgaatccact cctgatcctt acctttgtgg cggccgctct
    143 tgctgccccc 60
E--> 146 tttgatgatg atgacaagat cgttgggggc tattgtctag atacccctac
    147 gatgtgcccg 120
E--> 150 attacgccta gcggccgctt cccctttagtg agggttaatg cttcgagcag
```

same format error

RAW SEQUENCE LISTING   DATE: 01/03/2002
PATENT APPLICATION: US/10/015,989   TIME: 15:41:56

Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

```
      151 acatgataag 180
E--> 154 atacattgat gagtttggac aaaccacaac tagaatgcag tgaaaaaat
      155 gctttatttg 240
E--> 158 tgaaatttgt gatgctattg ctttatttgt aaccattata agctgcaata
      159 aacaagttga 300
      162 c
      168 <210> SEQ ID NO: 3
      171 <211> LENGTH: 484
      174 <212> TYPE: DNA
      177 <213> ORGANISM: ARTIFICIAL SEQUENCE
      183 <220> FEATURE:
      186 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
      189       VECTORS.
      195 <400> SEQUENCE: 3
E--> 198 gaattcacca ccatggacag caaaggttcg tcgcagaaat cccgcctgct
      199 cctgctgctg 60
E--> 202 gtggtgtcaa atctactctt gtgccagggt gtggtctccg actacaagga
      203 cgacgacgac 120
E--> 206 gtggacgcgg ccgctcttgc tgcccccttt atcgaggggc gcattgtgga
      207 gggctcggat 180
E--> 210 ctagataccc ctacgatgtg cccgattacg ccgctagata cccctacgat
      211 gtgcccgatt 240
E--> 214 acgccgctag ataccactac gatgtgcccg attacgccgc tagataccccc
      215 tacgatgtgc 300
E--> 218 ccgattacgc ctagcggccg cttccctttta gtgagggtta atgcttcgag
      219 cagacatgat 360
E--> 222 aagatacatt gatgagtttg gacaaaccac aactagaatg cagtgaaaaa
      223 aatgctttat 420
E--> 226 ttgtgaaatt tgtgatgcta ttgctttatt tgtaaccatt ataagctgca
      227 ataaacaagt 480
      230 tgac                                                       484
      236 <210> SEQ ID NO: 4
      239 <211> LENGTH: 382
      242 <212> TYPE: DNA
      245 <213> ORGANISM: ARTIFICIAL SEQUENCE
      251 <220> FEATURE:
      254 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
      257       VECTORS.
      263 <400> SEQUENCE: 4
E--> 266 gaattcacca ccatggacag caaaggttcg tcgcagaaat cccgcctgct
      267 cctgctgctg 60
E--> 270 gtggtgtcaa atctactctt gtgccagggt gtggtctccg actacaagga
      271 cgacgacgac 120
E--> 274 gtggacgcgg ccgctcttgc tgcccccttt gatgatgatg acaagatcgt
      275 tggggctac 180
E--> 278 aactgtctag acatcaccat caccatcact agcggccgct tccctttagt
      279 gagggttaat 240
E--> 282 gcttcgagca gacatgataa gatacattga tgagtttgga caaaccacaa
      283 ctagaatgca 300
```

301 –

same

same

same

RAW SEQUENCE LISTING   DATE: 01/03/2002
PATENT APPLICATION: US/10/015,989   TIME: 15:41:56

        Input Set : A:\ES.txt
        Output Set: N:\CRF3\01032002\J015989.raw

E--> 286 gtgaaaaaaa tgctttattt gtgaaatttg tgatgctatt gctttatttg   *same*
     287 taaccattat 360
     290 aagctgcaat aaacaagttg ac   382
     296 <210> SEQ ID NO: 5
     299 <211> LENGTH: 352
     302 <212> TYPE: DNA
     305 <213> ORGANISM: ARTIFICIAL SEQUENCE
     311 <220> FEATURE:
     314 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
     317   VECTORS.
     323 <400> SEQUENCE: 5
E--> 326 gaattcacca ccatggcttt cctctggctc ctctcctgct gggccctcct
     327 gggtaccacc 60
E--> 330 ttcggctgcg gggtccccga ctacaaggac gacgacgacg cggccgctct   *same*
     331 tgctgccccc 120
E--> 334 tttgatgatg atgacaagat cgttgggggc tatgctctag acatcaccat
     335 caccatcact 180
E--> 338 agcggccgct tccctttagt gagggttaat gcttcgagca gacatgataa
     339 gatacattga 240
E--> 342 tgagtttgga caaaccacaa ctagaatgca gtgaaaaaaa tgctttattt
     343 gtgaaatttg 300
E--> 346 tgatgctatt gctttatttg taaccattat aagctgcaat aaacaagttg
     347 ac   352
     353 <210> SEQ ID NO: 6
     356 <211> LENGTH: 385
     359 <212> TYPE: DNA
     362 <213> ORGANISM: ARTIFICIAL SEQUENCE
     368 <220> FEATURE:
     371 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
     374   VECTORS.
     380 <400> SEQUENCE: 6
E--> 383 gaattcacca ccatggcttt cctctggctc ctctcctgct gggccctcct
     384 gggtaccacc 60
E--> 387 ttcggctgcg gggtccccga ctacaaggac gacgacgacg cggccgctct
     388 tgctgccccc 120
E--> 391 tttgatgatg atgacaagat cgttgggggc tatgctctag atacccctac   *same*
     392 gatgtgcccg 180
E--> 395 attacgccgc tagacatcac catcaccatc actagcggcc gcttcccttt
     396 agtgagggtt 240
E--> 399 aatgcttcga gcagacatga taagatacat tgatgagttt ggacaaacca
     400 caactagaat 300
E--> 403 gcagtgaaaa aaatgcttta tttgtgaaat ttgtgatgct attgctttat
     404 ttgtaaccat 360
     407 tataagctgc aataaacaag ttgac   385
     413 <210> SEQ ID NO: 7
     416 <211> LENGTH: 1169
     419 <212> TYPE: DNA
     422 <213> ORGANISM: ARTIFICIAL SEQUENCE
     428 <220> FEATURE:

RAW SEQUENCE LISTING   DATE: 01/03/2002
PATENT APPLICATION: US/10/015,989   TIME: 15:41:56

Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

```
      431 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
      434         WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN
      440 <400> SEQUENCE: 7
E--> 443 gaattcacca ccatggacag caaaggttcg tcgcagaaat cccgcctgct
      444 cctgctgctg 60
E--> 447 gtggtgtcaa atctactctt gtgccagggt gtggtctccg actacaagga
      448 cgacgacgac 120
E--> 451 gtggacgcgg ccgctcttgc tgcccccttt gatgatgatg acaagatcgt
      452 tgggggctat 180
E--> 455 gctctagagg ccggtcagtg gccctggcag gtcagcatca cctatgaagg
      456 cgtccatgtg 240
E--> 459 tgtggtggct ctctcgtgtc tgagcagtgg gtgctgtcag ctgctcactg
      460 cttccccagc 300
E--> 463 gagcaccaca aggaagccta tgaggtcaag ctggggccc accagctaga
      464 ctcctactcc 360
E--> 467 gaggacgcca aggtcagcac cctgaaggac atcatccccc accccagcta
      468 cctccaggag 420
E--> 471 ggctcccagg gcgacattgc actcctccaa ctcagcagac ccatcacctt
      472 ctcccgctac 480
E--> 475 atccggccca tctgcctccc tgcagccaac gcctccttcc ccaacggcct
      476 ccactgcact 540
E--> 479 gtcactggct ggggtcatgt ggcccCCctca gtgagcctcc tgacgcccaa
      480 gccactgcag 600
E--> 483 caactcgagg tgcctctgat cagtcgtgag acgtgtaact gcctgtacaa
      484 catcgacgcc 660
E--> 487 aagcctgagg agccgcactt tgtccaagag gacatggtgt gtgctggcta
      488 tgtggagggg 720
E--> 491 ggcaaggacg cctgccaggg tgactctggg ggcccactct cctgccctgt
      492 ggagggtctc 780
E--> 495 tggtacctga cgggcattgt gagctgggga gatgcctgtg gggcccgcaa
      496 caggcctggt 840
E--> 499 gtgtacactc tggcctccag ctatgcctcc tggatccaaa gcaaggtgac
      500 agaactccag 900
E--> 503 cctcgtgtgg tgccccaaac ccaggagtcc cagcccgaca gcaacctctg
      504 tggcagccac 960
E--> 507 ctggccttca gctctagaca tcaccatcac catcactagc ggccgcttcc
      508 ctttagtgag 1020
E--> 511 ggttaatgct tcgagcagac atgataagat acattgatga gtttggacaa
      512 accacaacta 1080
E--> 515 gaatgcagtg aaaaaaatgc tttatttgtg aaatttgtga tgctattgct
      516 ttatttgtaa 1140
      519 ccattataag ctgcaataaa caagttgac                          1169
      525 <210> SEQ ID NO: 8
      528 <211> LENGTH: 1142
      531 <212> TYPE: DNA
      534 <213> ORGANISM: ARTIFICIAL SEQUENCE
      540 <220> FEATURE:
      543 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
      546         WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN
```

RAW SEQUENCE LISTING   DATE: 01/03/2002
PATENT APPLICATION: US/10/015,989   TIME: 15:41:56

Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

```
      552 <400> SEQUENCE: 8
E--> 555 gaattcacca ccatggcttt cctctggctc ctctcctgct gggccctcct
      556 gggtaccacc 60
E--> 559 ttcggctgcg gggtccccga ctacaaggac gacgacgacg cggccgctct
      560 tgctgccccc 120
E--> 563 tttgatgatg atgacaagat cgttgggggc tatgctctag aggccggtca
      564 gtggccctgg 180
E--> 567 caggtcagca tcacctatga aggcgtccat gtgtgtggtg gctctctcgt
      568 gtctgagcag 240
E--> 571 tgggtgctgt cagctgctca ctgcttcccc agcgagcacc acaaggaagc
      572 ctatgaggtc 300
E--> 575 aagctggggg cccaccagct agactcctac tccgaggacg ccaaggtcag
      576 caccctgaag 360
E--> 579 gacatcatcc cccaccccag ctacctccag gagggctccc agggcgacat
      580 tgcactcctc 420
E--> 583 caactcagca gacccatcac cttctcccgc tacatccggc ccatctgcct
      584 ccctgcagcc 480
E--> 587 aacgcctcct tccccaacgg cctccactgc actgtcactg gctggggtca
      588 tgtggccccc 540
E--> 591 tcagtgagcc tcctgacgcc caagccactg cagcaactcg aggtgcctct
      592 gatcagtcgt 600
E--> 595 gagacgtgta actgcctgta caacatcgac gccaagcctg aggagccgca
      596 ctttgtccaa 660
E--> 599 gaggacatgg tgtgtgctgg ctatgtggag gggggcaagg acgcctgcca
      600 gggtgactct 720
E--> 603 gggggcccac tctcctgccc tgtggagggt ctctggtacc tgacgggcat
      604 tgtgagctgg 780
E--> 607 ggagatgcct gtggggcccg caacaggcct ggtgtgtaca ctctggcctc
      608 cagctatgcc 840
E--> 611 tcctggatcc aaagcaaggt gacagaactc cagcctcgtg tggtgcccca
      612 aacccaggag 900
E--> 615 tcccagcccg acagcaacct ctgtggcagc cacctggcct tcagctctag
      616 acatcaccat 960
E--> 619 caccatcact agcggccgct ccctttagt gagggttaat gcttcgagca
      620 gacatgataa 1020
E--> 623 gatacattga tgagtttgga caaaccacaa ctagaatgca gtgaaaaaaa
      624 tgctttattt 1080
E--> 627 gtgaaatttg tgatgctatt gctttatttg taaccattat aagctgcaat
      628 aaacaagttg 1140
      631 ac                                                     1142
      637 <210> SEQ ID NO: 9
      640 <211> LENGTH: 1049
      643 <212> TYPE: DNA
      646 <213> ORGANISM: ARTIFICIAL SEQUENCE
      652 <220> FEATURE:
      655 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
      658       WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN
      664 <400> SEQUENCE: 9
E--> 667 gaattcacca ccatggacag caaaggttcg tcgcagaaat cccgcctgct
```

RAW SEQUENCE LISTING   DATE: 01/03/2002
PATENT APPLICATION: US/10/015,989   TIME: 15:41:56

          Input Set : A:\ES.txt
          Output Set: N:\CRF3\01032002\J015989.raw

```
        668 cctgctgctg 60
E--> 671 gtggtgtcaa atctactctt gtgccagggt gtggtctccg actacaagga
        672 cgacgacgac 120
E--> 675 gtggacgcgg ccgctcttgc tgcccccttt gatgatgatg acaagatcgt
        676 tggggctac 180
E--> 679 aactgtctag aaccccattc gcagccttgg caggcggcct tgttccaggg
        680 ccagcaacta 240
E--> 683 ctctgtggcg gtgtccttgt aggtggcaac tgggtcctta cagctgccca
        684 ctgtaaaaaa 300
E--> 687 ccgaaataca cagtacgcct gggagaccac agcctacaga ataaagatgg
        688 cccagagcaa 360
E--> 691 gaaatacctg tggttcagtc catcccacac ccctgctaca acagcagcga
        692 tgtggaggac 420
E--> 695 cacaaccatg atctgatgct tcttcaactg cgtgaccagg catccctggg
        696 gtccaaagtg 480
E--> 699 aagcccatca gcctggcaga tcattgcacc cagcctggcc agaagtgcac
        700 cgtctcaggc 540
E--> 703 tggggcactg tcaccagtcc ccgagagaat tttcctgaca ctctcaactg
        704 tgcagaagta 600
E--> 707 aaaatctttc cccagaagaa gtgtgaggat gcttacccgg ggcagatcac
        708 agatggcatg 660
E--> 711 gtctgtgcag gcagcagcaa aggggctgac acgtgccagg gcgattctgg
        712 aggccccctg 720
E--> 715 gtgtgtgatg gtgcactcca gggcatcaca tcctggggct cagacccctg
        716 tgggaggtcc 780
E--> 719 gacaaacctg gcgtctatac caacatctgc cgctacctgg actggatcaa
        720 gaagatcata 840
E--> 723 ggcagcaagg gctctagaca tcaccatcac catcactagc ggccgcttcc
        724 ctttagtgag 900
E--> 727 ggttaatgct tcgagcagac atgataagat acattgatga gtttggacaa
        728 accacaacta 960
E--> 731 gaatgcagtg aaaaaaatgc tttatttgtg aaatttgtga tgctattgct
        732 ttatttgtaa 1020
        735 ccattataag ctgcaataaa caagttgac                             1049
        741 <210> SEQ ID NO: 10
        744 <211> LENGTH: 1052
        747 <212> TYPE: DNA
        750 <213> ORGANISM: ARTIFICIAL SEQUENCE
        756 <220> FEATURE:
        759 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
        762       WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN
        768 <400> SEQUENCE: 10
E--> 771 gaattcacca ccatggacag caaaggttcg tcgcagaaat cccgcctgct
        772 cctgctgctg 60
E--> 775 gtggtgtcaa atctactctt gtgccagggt gtggtctccg actacaagga
        776 cgacgacgac 120
E--> 779 gtggacgcgg ccgctcttgc tgcccccttt gatgatgatg acaagatcgt
        780 tggggctac 180
E--> 783 aactgtctag aaaagcactc ccagccctgg caggcagccc tgttcgagaa
```

```
        RAW SEQUENCE LISTING                    DATE: 01/03/2002
        PATENT APPLICATION:  US/10/015,989      TIME: 15:41:56

                Input Set : A:\ES.txt
                Output Set: N:\CRF3\01032002\J015989.raw

    784 gacgcggcta 240
E--> 787 ctctgtgggg cgacgctcat cgcccccaga tggctcctga cagcagccca
    788 ctgcctcaag 300
E--> 791 ccccgctaca tagttcacct ggggcagcac aacctccaga aggaggaggg
    792 ctgtgagcag 360
E--> 795 acccggacag ccactgagtc cttcccccac cccggcttca acaacagcct
    796 ccccaacaaa 420
E--> 799 gaccaccgca atgacatcat gctggtgaag atggcatcgc cagtctccat
    800 cacctgggct 480
E--> 803 gtgcgacccc tcaccctctc ctcacgctgt gtcactgctg caccagctg
    804 cctcatttcc 540
E--> 807 ggctgggggca gcacgtccag cccccagtta cgcctgcctc acaccttgcg
    808 atgcgccaac 600
E--> 811 atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat
    812 cacagacacc 660
E--> 815 atggtgtgtg ccagcgtgca ggaagggggc aaggactcct gccagggtga
    816 ctccgggggc 720
E--> 819 cctctggtct gtaaccagtc tcttcaaggc attatctcct ggggccagga
    820 tccgtgtgcg 780
E--> 823 atcacccgaa agcctggtgt ctacacgaaa gtctgcaaat atgtggactg
    824 gatccaggag 840
E--> 827 acgatgaaga acaattctag acatcaccat caccatcact agcggccgct
    828 tccctttagt 900
E--> 831 gagggttaat gcttcgagca gacatgataa gatacattga tgagtttgga
    832 caaaccacaa 960
E--> 835 ctagaatgca gtgaaaaaaa tgctttattt gtgaaatttg tgatgctatt
    836 gctttatttg 1020
    839 taaccattat aagctgcaat aaacaagttg ac                    1052
   1067 <210> SEQ ID NO: 12
   1070 <211> LENGTH: 319
   1073 <212> TYPE: PRT
   1076 <213> ORGANISM: ARTIFICIAL SEQUENCE
   1082 <220> FEATURE:
   1085 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
   1088        WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN
   1094 <400> SEQUENCE 12
   1097 MET ALA PHE LEU TRP LEU LEU SER CYS TRP ALA LEU LEU GLY THR THR
   1100  1               5                  10                  15
   1106 PHE GLY CYS GLY VAL PRO ASP TYR LYS ASP ASP ASP ASP ALA ALA ALA
   1109             20                  25                  30
   1115 LEU ALA ALA PRO PHE ASP ASP ASP ASP LYS ILE VAL GLY GLY TYR ALA
   1118             35                  40                  45
   1124 LEU GLU ALA GLY GLN TRP PRO TRP GLN VAL SER ILE THR TYR GLU GLY
   1127    50                  55                  60
   1133 VAL HIS VAL CYS GLY GLY SER LEU VAL SER GLU GLN TRP VAL LEU SER
   1136 65                  70                  75                  80
   1142 ALA ALA HIS CYS PHE PRO SER GLU HIS HIS LYS GLU ALA TYR GLU VAL
   1145             85                  90                  95
   1151 LYS LEU GLY ALA HIS GLN LEU ASP SER TYR SER GLU ASP ALA LYS VAL
```

(handwritten annotations in right margin: "same", "see p. 8, too", "Per Sequence Rules (1.822) only the first letter of amino acid is in upper-case. e.g. Met Ala")

RAW SEQUENCE LISTING   DATE: 01/03/2002
PATENT APPLICATION: US/10/015,989   TIME: 15:41:56

Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

```
     1154              100                105                110
     1160 SER THR LEU LYS ASP ILE ILE PRO HIS PRO SER TYR LEU GLN GLU GLY
     1163              115                120                125
     1169 SER GLN GLY ASP ILE ALA LEU LEU GLN LEU SER ARG PRO ILE THR PHE
     1172        130                135                140
     1178 SER ARG TYR ILE ARG PRO ILE CYS LEU PRO ALA ALA ASN ALA SER PHE
     1181 145                150                155                160
     1187 PRO ASN GLY LEU HIS CYS THR VAL THR GLY TRP GLY HIS VAL ALA PRO
     1190              165                170                175
     1196 SER VAL SER LEU LEU THR PRO LYS PRO LEU GLN GLN LEU GLU VAL PRO
     1199              180                185                190
     1205 LEU ILE SER ARG GLU THR CYS ASN CYS LEU TYR ASN ILE ASP ALA LYS
     1208              195                200                205
     1214 PRO GLU GLU PRO HIS PHE VAL GLN GLU ASP MET VAL CYS ALA GLY TYR
     1217        210                215                220
     1223 VAL GLU GLY GLY LYS ASP ALA CYS GLN GLY ASP SER GLY GLY PRO LEU
     1226 225                230                235                240
     1232 SER CYS PRO VAL GLU GLY LEU TRP TYR LEU THR GLY ILE VAL SER TRP
     1235              245                250                255
     1241 GLY ASP ALA CYS GLY ALA ARG ASN ARG PRO GLY VAL TYR THR LEU
E--> 1242 ALA
E--> 1245              260                265                270
     1251 SER SER TYR ALA SER TRP ILE GLN SER LYS VAL THR GLU LEU GLN PRO
E--> 1254              275                280                285
     1260 ARG VAL VAL PRO GLN THR GLN GLU SER GLN PRO ASP SER ASN LEU CYS
E--> 1263        290                295                300
     1269 GLY SER HIS LEU ALA PHE SER SER ARG HIS HIS HIS HIS HIS
E--> 1272 305                310                315
     2409 <210> SEQ ID NO: 35
     2412 <211> LENGTH: 55
     2415 <212> TYPE: DNA
     2418 <213> ORGANISM: ARTIFICIAL SEQUENCE
     2424 <220> FEATURE:
     2427 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
     2430        OLIGONUCLEOTIDE
     2436 <400> SEQUENCE: 35
E--> 2439 aattcaccac catggctttc ctctggctcc tctcctgctg ggccctcctg
     2440 ggtac          55
     2446 <210> SEQ ID NO: 36
     2449 <211> LENGTH: 47
     2452 <212> TYPE: DNA
     2455 <213> ORGANISM: ARTIFICIAL SEQUENCE
     2461 <220> FEATURE:
     2464 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
     2467        OLIGONUCLEOTIDE
     2473 <400> SEQUENCE: 36
E--> 2476 ccaggagggc ccagcaggag aggagccaga ggaaagccat ggtggtg
     2477 47
     2483 <210> SEQ ID NO: 37
```

[handwritten annotations in right margin: "convert last two letters of amino acids to lower-case letters", "move up", "move up - see item 1 on Error Summary Sheet", "same error"]

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PATENT APPLICATION: US/10/015,989   TIME: 15:41:56

Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

```
   2486 <211> LENGTH: 45
   2489 <212> TYPE: DNA
   2492 <213> ORGANISM: ARTIFICIAL SEQUENCE
   2498 <220> FEATURE:
   2501 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
   2504       OLIGONUCLEOTIDE
   2510 <400> SEQUENCE: 37
E-->  2513 caccttcggc tgcggggtcc ccgactacaa ggacgacgac gacgc      same
   2514 45
   2520 <210> SEQ ID NO: 38
   2523 <211> LENGTH: 53
   2526 <212> TYPE: DNA
   2529 <213> ORGANISM: ARTIFICIAL SEQUENCE
   2535 <220> FEATURE:
   2538 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
   2541       OLIGONUCLEOTIDE
   2547 <400> SEQUENCE: 38
E-->  2550 ggccgcgtcg tcgtcgtcct tgtagtcggg gaccccgcag ccgaaggtgg   same
   2551 tac       53
   2629 <210> SEQ ID NO: 41
   2632 <211> LENGTH: 55
   2635 <212> TYPE: DNA
   2638 <213> ORGANISM: ARTIFICIAL SEQUENCE
   2644 <220> FEATURE:
   2647 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
   2650 -     OLIGONUCLEOTIDE
   2656 <400> SEQUENCE: 41
E-->  2659 ggccgctctt gctgccccct ttgatgatga tgacaagatc gttgggggct   same
   2660 atgct     55
   2666 <210> SEQ ID NO: 42
   2669 <211> LENGTH: 55
   2672 <212> TYPE: DNA
   2675 <213> ORGANISM: ARTIFICIAL SEQUENCE
   2681 <220> FEATURE:
   2684 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
   2687       OLIGONUCLEOTIDE
   2693 <400> SEQUENCE: 42
E-->  2696 ctagagcata gcccccaacg atcttgtcat catcatcaaa gggggcagca   same
   2697 agagc     55
   2703 <210> SEQ ID NO: 43
   2706 <211> LENGTH: 55
   2709 <212> TYPE: DNA
   2712 <213> ORGANISM: ARTIFICIAL SEQUENCE
   2718 <220> FEATURE:
   2721 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
   2724       OLIGONUCLEOTIDE
   2730 <400> SEQUENCE: 43
E-->  2733 ggccgctctt gctgccccct ttgatgatga tgacaagatc gttgggggct   same
   2734 attgt     55
```

RAW SEQUENCE LISTING   DATE: 01/03/2002
PATENT APPLICATION: US/10/015,989   TIME: 15:41:56

Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

```
      2740 <210> SEQ ID NO: 44
      2743 <211> LENGTH: 55
      2746 <212> TYPE: DNA
      2749 <213> ORGANISM: ARTIFICIAL SEQUENCE
      2755 <220> FEATURE:
      2758 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
      2761       OLIGONUCLEOTIDE
      2767 <400> SEQUENCE: 44
E-->  2770 ctagacaata gcccccaacg atcttgtcat catcatcaaa gggggcagca
      2771 agagc       55
      2777 <210> SEQ ID NO: 45
      2780 <211> LENGTH: 52
      2783 <212> TYPE: DNA
      2786 <213> ORGANISM: ARTIFICIAL SEQUENCE
      2792 <220> FEATURE:
      2795 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
      2798       OLIGONUCLEOTIDE
      2804 <400> SEQUENCE: 45
E-->  2807 ggccgctctt gctgcccct ttatcgaggg gcgcattgtg gagggctcgg
      2808 at          52
      2814 <210> SEQ ID NO: 46
      2817 <211> LENGTH: 52
      2820 <212> TYPE: DNA
      2823 <213> ORGANISM: ARTIFICIAL SEQUENCE
      2829 <220> FEATURE:
      2832 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
      2835       OLIGONUCLEOTIDE
      2841 <400> SEQUENCE: 46
E-->  2844 ctagatccga gccctccaca atgcgcccct cgataaaggg ggcagcaaga
      2845 gc          52
      3280 <210> SEQ ID NO: 54
      3283 <211> LENGTH: 284
      3286 <212> TYPE: PRT
      3289 <213> ORGANISM: ARTIFICIAL SEQUENCE
      3295 <220> FEATURE:
      3298 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: HUMAN MH2
      3301       PROTEASE IN PFEK ZYMOGEN VECTOR
      3307 <400> SEQUENCE: 54
      3310 MET ASP SER LYS GLY SER SER GLN LYS SER ARG LEU LEU LEU LEU LEU
      3313  1               5                  10                15
      3319 VAL VAL SER ASN LEU LEU LEU CYS GLN GLY VAL VAL SER ASP TYR LYS
      3322              20                  25                 30
      3328 ASP ASP ASP ASP VAL ASP ALA ALA ALA LEU ALA ALA PRO PHE ASP ASP
      3331          35                  40                  45
      3337 ASP ASP LYS ILE VAL GLY GLY TYR ASN CYS LEU GLU PRO HIS SER GLN
      3340      50                  55                  60
      3346 PRO TRP GLN ALA ALA LEU VAL MET GLU ASN GLU LEU PHE CYS SER GLY
      3349  65                  70                  75                 80
      3355 VAL LEU VAL HIS PRO GLN TRP VAL LEU SER ALA ALA HIS CYS PHE GLN
```

same

same

same

please edit amino acid letters

RAW SEQUENCE LISTING   DATE: 01/03/2002
PATENT APPLICATION: US/10/015,989   TIME: 15:41:56

Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

```
       3358                  85                  90                  95
       3364 ASN SER TYR THR ILE GLY LEU GLY LEU HIS SER LEU GLU ALA ASP GLN
       3367                 100               105               110
       3373 GLU PRO GLY SER GLN MET VAL GLU ALA SER LEU SER VAL ARG HIS PRO
       3376                 115               120               125
       3382 GLU TYR ASN ARG PRO LEU LEU ALA ASN ASP LEU MET LEU ILE LYS LEU
       3385           130               135               140
       3391 ASP GLU SER VAL SER GLU SER ASP THR ILE ARG SER ILE SER ILE ALA
       3394 145                 150               155                 160
       3400 SER GLN CYS PRO THR ALA GLY ASN SER CYS LEU VAL SER GLY TRP GLY
       3403                 165               170               175
       3409 LEU LEU ALA ASN GLY ARG MET PRO THR VAL LEU GLN CYS VAL ASN
E--> 3410 VAL
E--> 3413                 180               185               190
       3419 SER VAL VAL SER GLU GLU VAL CYS SER LYS LEU TYR ASP PRO LEU TYR
E--> 3422           195               200               205
       3428 HIS PRO SER MET PHE CYS ALA GLY GLY GLY HIS ASP GLN LYS ASP SER
E--> 3431      210               215               220
       3437 CYS ASN GLY ASP SER GLY GLY PRO LEU ILE CYS ASN GLY TYR LEU GLN
E--> 3440 225               230               235                 240
       3446 GLY LEU VAL SER PHE GLY LYS ALA PRO CYS GLY GLN VAL GLY VAL PRO
E--> 3449           245               250               255
       3455 GLY VAL TYR THR ASN LEU CYS LYS PHE THR GLU TRP ILE GLU LYS THR
E--> 3458           260               265               270
       3464 VAL GLN ALA SER SER ARG HIS HIS HIS HIS HIS HIS
E--> 3467      275               280
       3608 <210> SEQ ID NO: 59
       3611 <211> LENGTH: 1103
       3614 <212> TYPE: DNA
       3617 <213> ORGANISM: ARTIFICIAL SEQUENCE
       3623 <220> FEATURE:
       3626 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: NUCLEIC ACID
       3629      SEQUENCE OF HUMAN PROTEASE F IN CFEK2 ZYMOGEN
       3632      VECTOR
       3638 <400> SEQUENCE: 59
E--> 3641 gaattcacca ccatggcttt cctctggctc ctctcctgct gggccctcct
       3642 gggtaccacc 60
E--> 3645 ttcggctgcg gggtccccga ctacaaggac gacgacgacg cggccgctct
       3646 tgctgccccc 120
E--> 3649 tttgatgatg atgacaagat cgttgggggc tatgctctag aactcgggcg
       3650 ttggccgtgg 180
E--> 3653 caggggagcc tgcgcctgtg ggattcccac gtatgcggag tgagcctgct
       3654 cagccaccgc 240
E--> 3657 tgggcactca cggcggcgca ctgctttgaa acctatagtg accttagtga
       3658 tccctccggg 300
E--> 3661 tggatggtcc agtttggcca gctgacttcc atgccatcct tctggagcct
       3662 gcaggcctac 360
E--> 3665 tacaaccgtt acttcgtatc gaatatctat ctgagccctc gctacctggg
       3666 gaattcaccc 420
```

RAW SEQUENCE LISTING   DATE: 01/03/2002
PATENT APPLICATION: US/10/015,989   TIME: 15:41:56

Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

```
E--> 3669 tatgacattg ccttggtgaa gctgtctgca cctgtcacct acactaaaca
     3670 catccagccc 480
E--> 3673 atctgtctcc aggcctccac atttgagttt gagaaccgga cagactgctg
     3674 ggtgactggc 540
E--> 3677 tggggtaca  tcaaagagga tgaggcactg ccatctcccc acaccctcca
     3678 ggaagttcag 600
E--> 3681 gtcgccatca taaacaactc tatgtgcaac cacctcttcc tcaagtacag
     3682 tttccgcaag 660
E--> 3685 gacatctttg gagacatggt ttgtgctggc aatgcccaag gcgggaagga
     3686 tgcctgcttc 720
E--> 3689 ggtgactcag gtggacccтt ggcctgtaac aagaatggac tgtggtatca
     3690 gattggagtc 780
E--> 3693 gtgagctggg gagtgggctg tggtcggccc aatcggcccg gtgtctacac
     3694 caatatcagc 840
E--> 3697 caccactttg agtggatcca gaagctgatg gcccagagtg gcatgtccca
     3698 gccagacccc 900
E--> 3701 tcctggtcta gacatcacca tcaccatcac tagcggccgc ttcccttтag
     3702 tgagggttaa 960
E--> 3705 tgcttcgagc agacatgata agatacattg atgagtttgg acaaaccaca
     3706 actagaatgc 1020
E--> 3709 agtgaaaaaa atgctttatt tgtgaaattt gtgatgctat tgctttattt
     3710 gtaaccatta 1080
     3713 taagctgcaa taaacaagtt gac
```

                                                                          1103

peat the Sequence Listing to incure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY   DATE: 01/03/2002
PATENT APPLICATION: US/10/015,989   TIME: 15:41:57

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\01032002\J015989.raw**

```
L:31 M:270 C: Current Application Number differs, Replaced Application Number
L:34 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:82 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:1
L:82 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=1
M:254 Repeated in SeqNo=1
L:142 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:2
M:112 Repeated in SeqNo=2
M:254 Repeated in SeqNo=2
L:198 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:3
M:112 Repeated in SeqNo=3
M:254 Repeated in SeqNo=3
L:266 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:4
M:112 Repeated in SeqNo=4
M:254 Repeated in SeqNo=4
L:326 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:5
M:112 Repeated in SeqNo=5
M:254 Repeated in SeqNo=5
L:383 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:6
M:112 Repeated in SeqNo=6
M:254 Repeated in SeqNo=6
L:443 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:7
M:112 Repeated in SeqNo=7
M:254 Repeated in SeqNo=7
L:555 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:8
M:112 Repeated in SeqNo=8
M:254 Repeated in SeqNo=8
L:667 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:9
M:112 Repeated in SeqNo=9
M:254 Repeated in SeqNo=9
L:771 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:10
M:112 Repeated in SeqNo=10
M:254 Repeated in SeqNo=10
L:1242 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12
M:332 Repeated in SeqNo=12
L:1719 M:112 C: (48) String data converted to lower case,
L:1755 M:112 C: (48) String data converted to lower case,
L:1791 M:112 C: (48) String data converted to lower case,
L:1827 M:112 C: (48) String data converted to lower case,
L:1863 M:112 C: (48) String data converted to lower case,
L:1899 M:112 C: (48) String data converted to lower case,
L:1935 M:112 C: (48) String data converted to lower case,
L:1971 M:112 C: (48) String data converted to lower case,
L:2007 M:112 C: (48) String data converted to lower case,
L:2043 M:112 C: (48) String data converted to lower case,
L:2079 M:112 C: (48) String data converted to lower case,
L:2115 M:112 C: (48) String data converted to lower case,
L:2151 M:112 C: (48) String data converted to lower case,
```

VERIFICATION SUMMARY   DATE: 01/03/2002
PATENT APPLICATION: US/10/015,989   TIME: 15:41:57

Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

L:2187 M:112 C: (48) String data converted to lower case,
L:2223 M:112 C: (48) String data converted to lower case,
L:2259 M:112 C: (48) String data converted to lower case,
L:2295 M:112 C: (48) String data converted to lower case,
L:2331 M:112 C: (48) String data converted to lower case,
L:2367 M:112 C: (48) String data converted to lower case,
L:2403 M:112 C: (48) String data converted to lower case,
L:2439 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:35
M:112 Repeated in SeqNo=35
L:2476 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:47 SEQ:36
M:112 Repeated in SeqNo=36
L:2513 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:45 SEQ:37
M:112 Repeated in SeqNo=37
L:2550 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:38
M:112 Repeated in SeqNo=38
L:2587 M:112 C: (48) String data converted to lower case,
L:2623 M:112 C: (48) String data converted to lower case,
L:2659 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:41
M:112 Repeated in SeqNo=41
L:2696 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:42
M:112 Repeated in SeqNo=42
L:2733 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:43
M:112 Repeated in SeqNo=43
L:2770 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:44
M:112 Repeated in SeqNo=44
L:2807 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:45
M:112 Repeated in SeqNo=45
L:2844 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:46
M:112 Repeated in SeqNo=46
L:2881 M:112 C: (48) String data converted to lower case,
L:2917 M:112 C: (48) String data converted to lower case,
L:2953 M:112 C: (48) String data converted to lower case,
L:2989 M:112 C: (48) String data converted to lower case,
L:3025 M:112 C: (48) String data converted to lower case,
L:3061 M:112 C: (48) String data converted to lower case,
L:3410 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:54
M:332 Repeated in SeqNo=54
L:3503 M:112 C: (48) String data converted to lower case,
L:3641 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:59
M:254 Repeated in SeqNo=59
L:3752 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:60
M:254 Repeated in SeqNo=60